

A

Oilgo #	Name	Primer Sequences (5'-3')
2663	mK1	TTG GTG CTG ATG TTC TGG
2664	mK2	ATC TTC TTG CTG TTC TGG
2665	mK3	TGG GTG CTG CTG CTC TGG
2666	mK4	GGG CTG CTT GTG CTC TGG
2667	mK5	GGA ATC TTG TTG CTC TGG
2668	mK6	RTR TTS CTG CTG CTR TGG
2669	mK7	GGT CTC CTG TTG CTC TGT
2670	mK8	ATA TTT CTA CTG CTC TGT
2671	mK9	GTC ATA ATR TCC AGA GGA

B

Oilgo #	Name	Primer Sequences (5'-3')
2672	mH1	CTG AGC TGT GTA TTC CT
2673	mH2	CTC ARM TTG ATT TTC CT
2674	mH3	TGG RTC ATS TTC TTC CT
2675	mH4	TKS RTC TTT CTC TTC CT
2676	mH5	TGT ATC ATS CTC TTC TT
2677	mH6	TGG RTC TTT CTC TTT TT
2678	mH7	TTA AAC TGG GTT TTT CT
2679	mH8	GKG CTG YTC YTC TGC CT
2680	mH9	TTA AGT CTT CTG TAC CTG
2730	MH11	TCAGTAACTGCAGGTGTCCA
2731	MH12	TTTTAAAAGGTGTCCAGTGT
2732	MH13	GCAACAGCTACAGGTGTCCA
2733	MH14	CAGCTACAGRTGTCCACTCC
2734	MH15	ATTCCAAGCTGTGTCCTGTCC
2735	MH16	CTCCTGTCAGGAACTGCAGGTGT
2736	MH17	CAGTGGTTACAGGGGTCAATTCA
2737	MH18	CTGTTSACAGCCHTTCKGGT
2738	MH19	CTGATGGCAGCTGCCCAAAGT
2739	MH20	TTTATCAAGGTGTGCATTGT

C

2650      5' TCACTGGATGGTGGGAAGATGGATACA 3'  
2656      5' GACATTTGGGAAGGACTGACTCTC 3'  
2706      5' CAG GGG GCT CTC GCA GGA GAC GAG 3'

FIGURE 1

Attorney Docket: P-IX 4976  
Inventors: Watkins et al.

HuIV-26 VL

GACATTGTGATGACACAGTCTCCATCTTTGTTGAGTGTGTCAGCAGGAGAGAAGGTCCT  
ATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCC  
TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTAGG  
GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACCGATTTCCTCTTATC  
ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGAATGATCATAGTTAT  
CCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA

FIGURE 2A

HuIV-26 VH

GAGGTGAAGCTTCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGAAACT  
CTCCTGTGCAGCCTCAGGATTTCGATTTTAGTAGATACTGGATGAGTTGGGTCCGGCAGG  
CTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGTACGATAAAC  
TATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCCAAAAATACGCT  
GTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTATTACTGTGCAAGAC  
CGGTTGATGGTTACTACGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC  
TCCTCA

FIGURE 2B

# Vk Domain

	1	10	20	30	40
HUIV26	D	I	V	M	T
	Q	S	P	S	L
	S	V	S	A	G
	E	K	V	T	M
	S	C	K	S	S
	Q	S	L	L	N
	S	G	N	Q	K
	N	Y	L	A	W
	Y	Q	K	P	G
	P	P	K	L	L
	I	I	I	I	I
VKIV	D	I	V	M	T
	Q	S	P	S	L
	A	V	S	L	G
	E	R	A	T	I
	N	C	K	S	S
	Q	S	V	L	Y
	S	S	N	N	K
	N	Y	L	A	W
	Y	Q	K	P	G
	P	P	K	L	L
	I	I	I	I	I
	50	60	70	80	90
HUIV26	G	A	S	T	R
	E	S	G	V	P
	D	R	F	T	G
	S	G	S	G	T
	D	F	T	L	I
	I	S	S	V	Q
	A	E	D	L	A
	V	Y	C	Q	N
	D	H	S	Y	P
	Y	T	F	G	G
	T	K	L	E	I
	K	I	K	I	K
VKIV/JK2	W	A	S	T	R
	E	S	G	V	P
	D	R	F	T	G
	S	G	S	G	T
	D	F	T	L	I
	S	S	L	Q	A
	E	D	V	A	V
	Y	C	Q	D	H
	S	Y	P	T	F
	G	G	T	K	L
	E	I	K	I	K

# VH Domain

	1	10	20	30	40
HUIV26	E	V	K	L	E
	S	G	G	L	V
	Q	P	G	G	S
	L	K	L	S	C
	A	A	S	G	F
	D	F	S	R	Y
	W	M	S	W	V
	R	Q	A	P	G
	K	G	L	E	W
	I	G	I	I	I
VHIII	E	V	Q	L	V
	E	S	G	G	L
	V	Q	P	G	S
	L	R	L	S	C
	A	A	S	G	F
	T	F	S	S	Y
	W	M	S	W	V
	R	Q	A	P	G
	K	G	L	E	W
	V	A	A	A	A
	50	60	70	80	90
HUIV26	E	I	N	P	D
	S	S	T	I	N
	Y	T	P	S	L
	K	D	K	F	I
	I	S	R	D	N
	A	K	N	T	L
	Y	L	Q	M	S
	K	V	R	S	E
	D	T	A	L	Y
	Y	C	A	R	A
VHIII	N	I	K	Q	D
	G	S	E	K	Y
	Y	V	D	S	V
	K	G	R	F	T
	I	S	R	D	N
	A	K	N	S	L
	Y	L	Q	M	N
	S	L	R	A	E
	D	T	A	V	Y
	C	A	R	A	R
	abc	abc	abc	abc	abc
	100	100	100	100	100
HUIV26	P	V	D	G	Y
	D	A	M	D	Y
	W	G	Q	G	T
	S	V	T	V	S
	S	S	S	S	S
JH6	P	D	Y	Y	Y
	Y	G	M	D	V
	W	G	Q	G	T
	T	V	T	V	S
	S	S	S	S	S

FIGURE 2C

HUI77 VL sequence

GATGTTTTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCC  
ATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAGAATGG  
TACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTT  
TCTGGTGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCAAGATC  
AGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTCAAGGTTACATGTTCCG  
TGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA

FIGURE 3A

HUI77 VH SEQUENCE

CAGGTTACTCTGAAAGAGACTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG  
ACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTAGGCTGGATTCGT  
CAGCCTTCAGGAGAGGGTCTAGAGTGGCTGGCAGACATTTGGTGGGATGACAATAAGTAC  
TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCCAGCAACCAGGTA  
TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACTTACTACTGTGCTCGAAGA  
GCTAACTATGGTAACCCCTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACC  
GTCTCCTCA

FIGURE 3B

Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

	50	60	70	80	90	100
HUI-77	<u>KVSNR</u> FSGVPDRFSGSGS	GTDTLLKISR	VEAEDLVYYCF	<u>QGS</u>	HPWTF	GGTKLEIK
VKII/JK1	TL	SYR	ASGVPDRFSGSGS	GTDTLLKISR	VEAEDVG	VYYC
					MQGS	HPWTF
					GGTK	VEIK

## FIGURE 3C

	50	60	70	80	abc	90
HUI-77	<u>DIWDDNKYYNPSLKSR</u>	<u>LTISKDTS</u>	<u>SNQVFLK</u>	<u>ITSVDT</u>	<u>ADTATYYCAR</u>	
VHII	<u>RIDWDDDKFYSTSLK</u>	<u>TRLTISKDTS</u>	<u>KNQVVL</u>	<u>TMTNMD</u>	<u>PVDATYYCAR</u>	
HUI-77	100cde	110				
	<u>RANYGNPYYAMD</u>	<u>YWGQGT</u>	<u>SVTVSS</u>			
JH6	RANYYYYY	AMDVWGQGT	TVTVSS			

HUI77 VL sequence

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
HUI77 VL	GAT	GTT	TTG	ATG	ACC	CAA	ACT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT
DPK13	---	A--	G--	---	---	--G	---	---	---	---	---	--C	---	-CC	-C-
	CDR1														
	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c
HUI77 VL	GGA	GAT	CAA	GCC	TCC	ATC	TCT	TGC	AGA	TCT	AGT	CAG	AGC	ATT	GTA
DPK13	---	--G	-CG	---	---	---	--C	---	--G	---	---	---	---	C-C	T-G
	27d	27e	27f	28	29	30	31	32	33	34	35	36	37	38	39
HUI77 VL	CAT	AGT	...	AAT	GGA	AAC	ACC	TAT	TTA	GAA	TGG	TAC	CTG	CAG	AAA
DPK13	G--	---	GAT	G--	---	---	---	---	--G	--C	---	---	---	---	--G
	CDR2														
	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54
HUI77 VL	CCA	GGC	CAG	TCT	CCA	AAG	CTC	CTG	ATC	TAC	AAA	GTT	TCC	AAC	CGA
DPK13	---	--G	---	---	---	C--	---	---	---	--T	-CG	C--	---	T-T	--G
	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69
HUI77 VL	TTT	TCT	GGT	GTC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGA	TCA	GGG	ACA
DPK13	GCC	---	--A	---	---	---	---	---	---	---	---	--G	---	--C	--T
	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84
HUI77 VL	GAT	TTC	ACA	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	GAG	GAT	CTG	GGA
DPK13	---	---	---	--G	--A	---	---	--G	---	---	---	---	---	G-T	---
	CDR3														
	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
HUI77 VL	GTT	TAT	TAC	TGC	TTT	CAA	GGT	TCA	CAT	GTT	CCG	TGG	ACG	TTC	GGT
DPK13	---	---	---	---	A-G	---	---	---	---	---	---	---	---	---	--C
	100	101	102	103	104	105	106	107							
HUI77 VL	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA							
JK1	CA-	--G	---	---	G--	---	---	---							

FIGURE 3D



HUIV26 LCDR3

IV26-I7.1 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC ATT MNN ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.2 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC MNN CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.3 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG MNN ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.4 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT MNN ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.5 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA MNN ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.6 CTT GGT CCC CTG GCC AAA AGT GTA CGG MNN ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.7 CTT GGT CCC CTG GCC AAA AGT GTA MNN ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.8 CTT GGT CCC CTG GCC AAA AGT MNN CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC  
IV26-I7.9 CTT GGT CCC CTG GCC AAA MNN GTA CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC

HUIV26 HCDR3

IV26-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC AAC MNN TCT CGC ACA GTA ATA CAC  
IV26-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC MNN CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC MNN AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA MNN ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA MNN ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC MNN GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC MNN GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.10 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC  
IV26-h7.11 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC

FIGURE 4A

Attorney Docket: P-IX 4976  
Inventors: Watkins et al.

HUIV26 LCDR1a

IV26L1-1 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTGGAMNNGCAGTTGATGGTGGCCCT  
IV26L1-2 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTMNNGCTGCAGTTGATGGTGGCCCT  
IV26L1-3 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGMNNGGACTTGCAGTTGATGGTGGCCCT  
IV26L1-4 GTTCTTTTGGTTTCCGCWGTTTAACAGACTMNNGCTGGACTTGCAGTTGATGGTGGCCCT  
IV26L1-5 GTTCTTTTGGTTTCCGCWGTTTAACAGMNNGCTGGCTGGACTTGCAGTTGATGGTGGCCCT  
IV26L1-6 GTTCTTTTGGTTTCCGCWGTTTAAMNNACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT  
IV26L1-7 GTTCTTTTGGTTTCCGCWGTTMNNAAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT  
IV26L1-8 GTTCTTTTGGTTTCCGCWMNNTAACAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT

HUIV26 LCDR1b

IV26L1-9 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTGGTTTCCMNNGTTTAAACAGACTCTGGCT  
IV26L1-10 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTGGTTMNGCWGTTTAAACAGACTCTGGCT  
IV26L1-11 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTGMNNTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-12 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTMNNGTTTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-13 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTMNNTTGGTTTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-14 TGGTTTCTGCTGGTACCAAGCTAAGTAMNNTTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-15 TGGTTTCTGCTGGTACCAAGCTAAMNNGTTCTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-16 TGGTTTCTGCTGGTACCAAGCMNNGTAGTTCTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT  
IV26L1-17 TGGTTTCTGCTGGTACCAMNNTAAGTAGTTCTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT

HUIV26 LCDR2

IV26L2-1 GAATCGGTCAGGGACCCCGGATTCCCTGGTAGATGCMNNGTAAATGAGCAGCTTAGG  
IV26L2-2 GAATCGGTCAGGGACCCCGGATTCCCTGGTAGAMNNGCGTAAATGAGCAGCTTAGG  
IV26L2-3 GAATCGGTCAGGGACCCCGGATTCCCTGGTMNNTGCCCGTAAATGAGCAGCTTAGG  
IV26L2-4 GAATCGGTCAGGGACCCCGGATTCCCTMNNAGATGCCCGTAAATGAGCAGCTTAGG  
IV26L2-5 GAATCGGTCAGGGACCCCGGATTMNNNGTAGATGCCCGTAAATGAGCAGCTTAGG  
IV26L2-6 GAATCGGTCAGGGACCCCGGAMNNGCTGGTAGATGCCCGTAAATGAGCAGCTTAGG  
IV26L2-7 GAATCGGTCAGGGACCCCMNNTTCCCTGGTAGATGCCCGTAAATGAGCAGCTTAGG

HUIV26 HCDR1

IV26H1-1 TGGAGCCTGGCGGACCCAGCTCATCCAATAMNNACTAAAGGTGAATCCAGA  
IV26H1-2 TGGAGCCTGGCGGACCCAGCTCATCCAMNNTCTACTAAAGGTGAATCCAGA  
IV26H1-3 TGGAGCCTGGCGGACCCAGCTCATMNNATATCTACTAAAGGTGAATCCAGA  
IV26H1-4 TGGAGCCTGGCGGACCCAGCTMNNCAATATCTACTAAAGGTGAATCCAGA  
IV26H1-5 TGGAGCCTGGCGGACCCAMNNCATCCAATATCTACTAAAGGTGAATCCAGA

HUIV26 HCDR2a

IV26H2-1 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTATMNNGCCAAYCCACTCCAGCCCTTTC  
IV26H2-2 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTMNNNTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-3 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGMNNTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-4 TAGAGATGGCGTATAGTTTATCGTACTGCTATCMNNATTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-5 TAGAGATGGCGTATAGTTTATCGTACTGCTMNNNTGGATTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-6 TAGAGATGGCGTATAGTTTATCGTACTMNNATCTGGATTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-7 TAGAGATGGCGTATAGTTTATCGTMNNGCTATCTGGATTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-8 TAGAGATGGCGTATAGTTTATMNNACTGCTATCTGGATTATTTCGCCAAYCCACTCCAGCCCTTTC  
IV26H2-9 TAGAGATGGCGTATAGTTMNNCGTACTGCTATCTGGATTATTTCGCCAAYCCACTCCAGCCCTTTC

HUIV26 HCDR2b

IV26H2-10 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGGCGTATAMNNTATCGTACTGCTATCTGG  
IV26H2-11 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGGCGTMNNGTTTATCGTACTGCTATCTGG  
IV26H2-12 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGGMNNTAGTTTATCGTACTGCTATCTGG  
IV26H2-13 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGAMNNGTATAGTTTATCGTACTGCTATCTGG  
IV26H2-14 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGMNNNTGGCGTATAGTTTATCGTACTGCTATCTGG  
IV26H2-15 CGTTGTCTCTGGAGATGRTGAATYTATCCTTMNNAGATGGCGTATAGTTTATCGTACTGCTATCTGG  
IV26H2-16 CGTTGTCTCTGGAGATGRTGAATYTATCMNNNTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG  
IV26H2-17 CGTTGTCTCTGGAGATGRTGAATYTAMNNTTTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG

FIGURE 4B

Beneficial Mutations for HuIV-26 Antibody

CDRs	H1	H2	H3	L1	L2	L3
Kabat Number	31 34 35	57 62 64 65	97 98 102	27 27d 27e 27f 29		93 94
HuIV-26	R M S	I S K D	D G Y	Q N S G Q		S Y
Mutations	H I T A G	A Y Q S S A H G	P P P G A N T H A	R S Y Y K S W R H H R I		Q N G S L P A M T V

FIGURE 4C

Attorney Docket: P-IX 4976  
Inventors: Watkins et al.

### HUI77 LCDR3

177-17.1 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC TTG MNN GCA GTA ATA AAC TCC AAC ATC  
177-17.2 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC MNN AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.3 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA MNN TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.4 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG MNN ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.5 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC MNN TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.6 CTT GGT GCC CTG GCC GAA CGT CCA CGG MNN ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.7 CTT GGT GCC CTG GCC GAA CGT CCA MNN AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.8 CTT GGT GCC CTG GCC GAA CGT MNN CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC  
177-17.9 CTT GGT GCC CTG GCC GAA MNN CCA CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC

### HUI77 HCDR3

177-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC MNN TCG AGC ACA GTA ATA CGT  
177-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT MNN TCT TCG AGC ACA GTA ATA CGT  
177-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA MNN AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC MNN GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT MNN ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG MNN ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA MNN GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA MNN GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC MNN GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.10 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.11 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.12 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT  
177-h7.13 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT

FIGURE 5A

HUI77 LCDR1a

3000 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT AGA MNN GCA GGA GAT GGA GGC C  
3001 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT MNN CCT GCA GGA GAT GGA GGC C  
3002 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG MNN AGA CCT GCA GGA GAT GGA GGC C  
3003 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT MNN ACT AGA CCT GCA GGA GAT GGA GGC C  
3004 ATA GGT GTT TCC ATT ACT ATG TAC AAT MNN CTG ACT AGA CCT GCA GGA GAT GGA GGC C  
3005 ATA GGT GTT TCC ATT ACT ATG TAC MNN GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C  
3006 ATA GGT GTT TCC ATT ACT ATG MNN AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C  
3007 ATA GGT GTT TCC ATT ACT MNN TAC AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C

HUI77 LCDR1b

3008 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC ATT MNN ATG TAC AAT GCT CTG ACT  
3009 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC MNN ACT ATG TAC AAT GCT CTG ACT  
3010 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT MNN ATT ACT ATG TAC AAT GCT CTG ACT  
3011 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT MNN TCC ATT ACT ATG TAC AAT GCT CTG ACT  
3012 TGG CTT CTG CAG GTA CCA TTC CAA ATA MNN GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT  
3013 TGG CTT CTG CAG GTA CCA TTC CAA MNN GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT  
3014 TGG CTT CTG CAG GTA CCA TTC MNN ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT  
3015 TGG CTT CTG CAG GTA CCA MNN CAA ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT

HUI77 LCDR2

3016 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA AAC MNN ATA GAT CAG GAG CTG TGG  
3017 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA MNN TTT ATA GAT CAG GAG CTG TGG  
3018 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT MNN AAC TTT ATA GAT CAG GAG CTG TGG  
3019 GAA CCT GTC TGG GAC TCC AGA AAA CCG MNN GGA AAC TTT ATA GAT CAG GAG CTG TGG  
3020 GAA CCT GTC TGG GAC TCC AGA AAA MNN GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG  
3021 GAA CCT GTC TGG GAC TCC AGA MNN CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG  
3022 GAA CCT GTC TGG GAC TCC MNN AAA CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG

HUI77 HCDR1

3023 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC AGA MNN GCT GAG TGA GAA CCC AGA  
3024 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC MNN AGT GCT GAG TGA GAA CCC AGA  
3025 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT MNN AGA AGT GCT GAG TGA GAA CCC AGA  
3026 TGG GGG CTG ACG GAT CCA GCC CAC ACC MNN TCC AGA AGT GCT GAG TGA GAA CCC AGA  
3027 TGG GGG CTG ACG GAT CCA GCC CAC MNN CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA  
3028 TGG GGG CTG ACG GAT CCA GCC MNN ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA  
3029 TGG GGG CTG ACG GAT CCA MNN CAC ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA

HUI77 HCDR2a

3038 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA AAT MNN TGC AAG CCA CTC CAG GGC  
3039 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA MNN GTC TGC AAG CCA CTC CAG GGC  
3040 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA MNN AAT GTC TGC AAG CCA CTC CAG GGC  
3041 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC MNN CCA AAT GTC TGC AAG CCA CTC CAG GGC  
3042 CAG AGA TGG GTT GTA GTA TTT ATT GTC MNN CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC  
3043 CAG AGA TGG GTT GTA GTA TTT ATT MNN ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC  
3044 CAG AGA TGG GTT GTA GTA TTT MNN GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC  
3045 CAG AGA TGG GTT GTA GTA MNN ATT GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC

HUI77 HCDR2b

3030 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT GTA MNN TTT ATT GTC ATC CCA CCA  
3031 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT MNN GTA TTT ATT GTC ATC CCA CCA  
3032 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG MNN GTA GTA TTT ATT GTC ATC CCA CCA  
3033 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA MNN GTT GTA GTA TTT ATT GTC ATC CCA CCA  
3034 CTT GGA GAT GGT GAG CCT GCT CTT CAG MNN TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA  
3035 CTT GGA GAT GGT GAG CCT GCT CTT MNN AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA  
3036 CTT GGA GAT GGT GAG CCT GCT MNN CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA  
3037 CTT GGA GAT GGT GAG CCT MNN CTT CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA

FIGURE 5B

Beneficial Mutations for HuI-77 Antibody

CDRs	H1	H2	H3	L1	L2	L3
Kabat Number	32 35b	59 64	95 100 100e 102	27c 27d 27e 28 30 33	50 51 53 54 56	89 90 91 92 93 94 97
HuI-77	S G	Y K	R N M Y	V H S N N L	K V N R S	F Q G S H V T
Mutations	P W W L A	S P A P	P V Q K Q W N T M L T H V	P L W Y Y F W S W V	S A S L W F	V R S W L T A H W E T S H K I Q

FIGURE 5C

Beneficial mutations chosen for combinatorial library

CDRs	H1	H2	H3	L1	L3	SPEkon	SPEkoff
Kabat Number	35	57 62	102	27d 27e 27f	93	O.D.560	O.D.560
wild type	S	I S	Y	N S G	S		
HuIV-26	S	I S	Y	N S G	S		
Mutations	T A	A Y A H	P	S Y Y W R H H R	Q		

Beneficial mutants

4.1-2D4	S	I S	P	N S G	Q		
L1b-F11	S	I S	P	N S Y	Q	0.745	0.483
H2a-G8	S	A S	P	N S G	Q	0.397	0.159
2D4H1-C3	A	I S	P	N S G	Q		
DcomA4	S	A Y	P	N Y Y	Q	0.981	0.769
DcomB1	A	A Y	P	N Y H	Q	1.018	0.714
DcomE1						1.031	0.758
DcomH2						1.07	0.705
DcomD2	S	A S	P	N R Y	Q	1.104	0.729
DcomD3	T	A Y	P	N S Y	Q	1.035	0.736
DcomD6	S	A Y	P	N W Y	Q	1.102	0.753
DcomA11						1.003	0.786
DcomE3	T	A Y	P	N R Y	Q	0.991	0.754
DcomG2	A	A Y	P	N R Y	Q	1.161	0.856
DcomA7	T	V S	P	N Y Y	Q	0.986	0.77
DcomB8	T	A A	P	N W Y	Q	0.998	0.807
DcomA2						1.026	0.74
DcomB10	T	A H	P	N W Y	Q	0.87	0.735
DcomC8	S	A A	P	N W Y	Q	0.978	0.763
DcomD7	T	A Y	P	N W Y	Q	1.083	0.794
DhuG5							
DhuH8							
DcomD11	A	A A	P	N W H	Q	1.125	0.752
DcomE11	A	A H	P	N W H	Q	0.973	0.732

Primers for combinatorial mutation

dH5762 TCTCTGGAGATGGTGAATTTACGTACTGCTATCTGGATT  
dL27def CTAAGTAGTTCTTTTGGTTGTTATAACAGACTCTGGCTGGA  
H1-35 TGGAGCCTGGCGGACCCAGGHCATCCAATATCTACTAAAGGTGAATCCAGA  
H2-5762a TCTCTGGAGATGGTGAATCTATCCTTTAGGGM TGGCGTATAGTTGGCCGTA CTGCTATCTGGATT  
H2-5762b TCTCTGGAGATGGTGAATCTATCCTTTAGGTR TGGCGTATAGTTGGCCGTA CTGCTATCTGGATT  
L1-27def1 CTAAGTAGTTCTTTTGGTTGTRGTRGYTTAACAGACTCTGGCTGGA  
L1-27def2 CTAAGTAGTTCTTTTGGTTGCSGTRGYTTAACAGACTCTGGCTGGA  
L1-27def3 CTAAGTAGTTCTTTTGGTTGTRGCKGYTTAACAGACTCTGGCTGGA  
L1-27def4 CTAAGTAGTTCTTTTGGTTGCSGCKGYTTAACAGACTCTGGCTGGA  
L1-27def5 CTAAGTAGTTCTTTTGGTTGTRCCAGYTTAACAGACTCTGGCTGGA  
L1-27def6 CTAAGTAGTTCTTTTGGTTGCSCCAGYTTAACAGACTCTGGCTGGA

FIGURE 6

Beneficial mutations chosen for combinatorial library

CDRs	H1	H2	H3	L1	L3	Screen	Screen
Kabat Number	32 35b	59	100e	27d 28 33	91 94	kon	koff
wild type	S G	Y	M	H N L	G V		
HuI-77	S G	Y	M	H N L	V		
Mutations	P W L A	S A P	Q	L Y F S W	S		

Beneficial combinatorial mutants

Qh2b-B7	S G	A	Q	H N L	S		
QH2b-A3	S G	S	Q	H N L			
Qcom1B6	P W	S	Q	S W L	S	1.319	0.534
Qcom1B8	P W	S	Q	S Y L	S	1.266	0.497
Qcom1E7						1.247	0.46
Qcom1G10						1.282	0.452
Qcom2G2						1.304	0.402
Qcom1C3	P W	A	Q	S W L	S	1.342	0.535
Qcom2A2						1.605	0.647
Qcom1G3						1.274	0.464
Qcom1D3	P W	T	Q	S W L	S	1.647	0.984
QhuD9							
QhuD93							
Qcom1E3	P W	A	Q	S Q L	S	1.225	0.347
Qcom2F6						1.311	0.321
Qcom1H6	P W	S	Q	S Q L	S	1.295	0.323
Qcom1H7	P W	A	Q	H Q F	S F	1.634	1.08
Qcom2A4	P A	A	Q	S Y L	S	1.304	0.265
Qcom2B11	P W	A	Q	H Y L	S	1.11	0.221
Qcom2C1	P W	Y	Q	S W F	S	1.189	0.213
Qcom2D9	P W	S	Q	H W L	S	1.101	0.209
Qcom2E3	P W	A	Q	H W L	S	1.117	0.248

Primers for combinatorial mutation

dL27d-33 CTT CTG CAG GTA CCA TTC GTTA TAC AAT GCT CTG ACT AGA

H1-35b1 TGG GGG CTG ACG GAT CCA CMA CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA

H1-35b2 TGG GGG CTG ACG GAT CCA GSC CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA

H2-59 GCT CTT CAG AGA TGG GTT AGV GTA TTT ATT GTC ATC CCA C

L27d1 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT CRA TAC AAT GCT CTG ACT AGA

L27d2 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT CRA TAC AAT GCT CTG ACT AGA

L27d3 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT CRA TAC AAT GCT CTG ACT AGA

L27d4 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT GTG TAC AAT GCT CTG ACT AGA

L27d5 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT GTG TAC AAT GCT CTG ACT AGA

L27d6 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT GTG TAC AAT GCT CTG ACT AGA

FIGURE 7



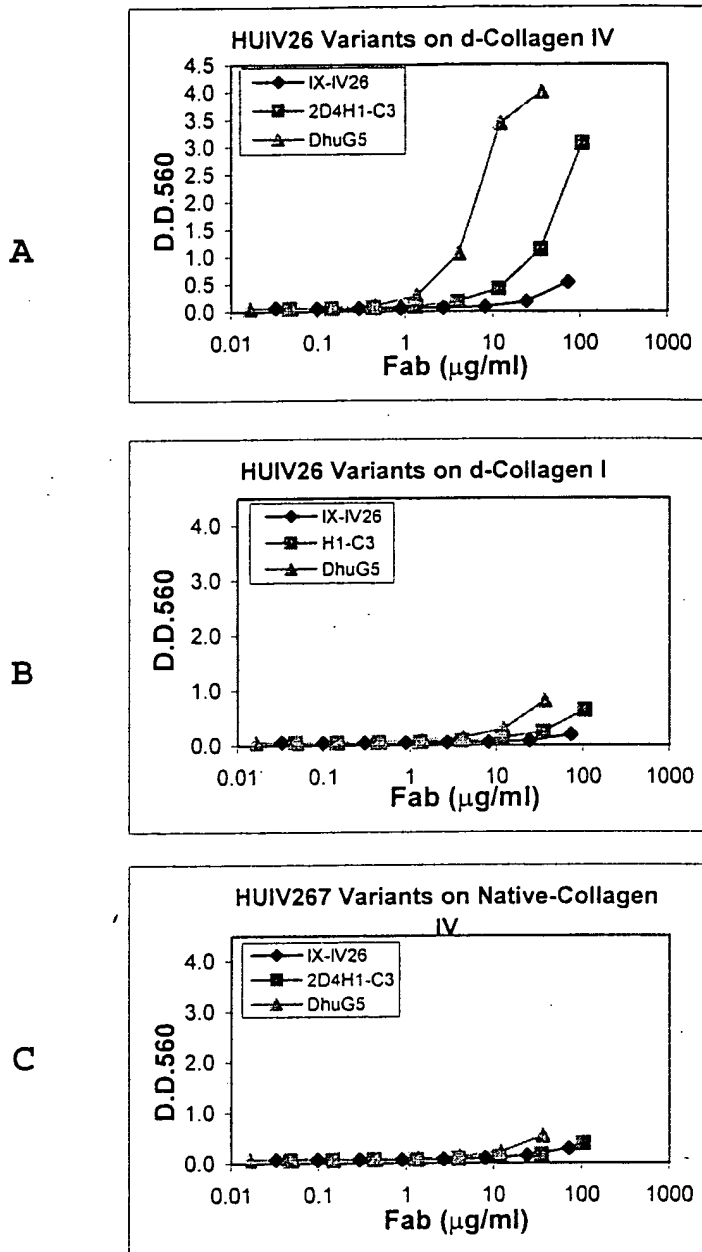
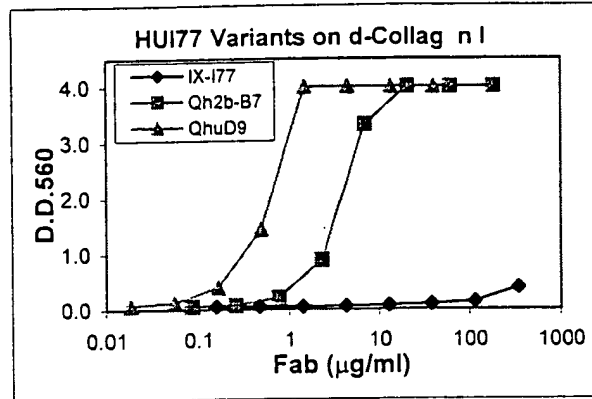
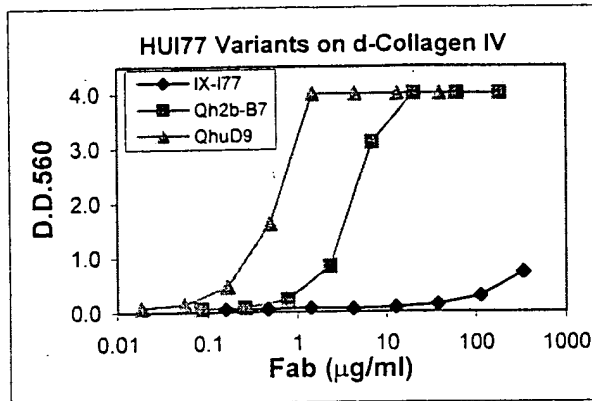


FIGURE 8

A



B



C

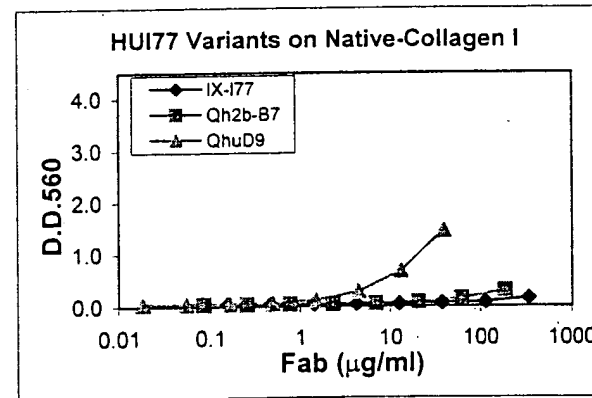


FIGURE 9

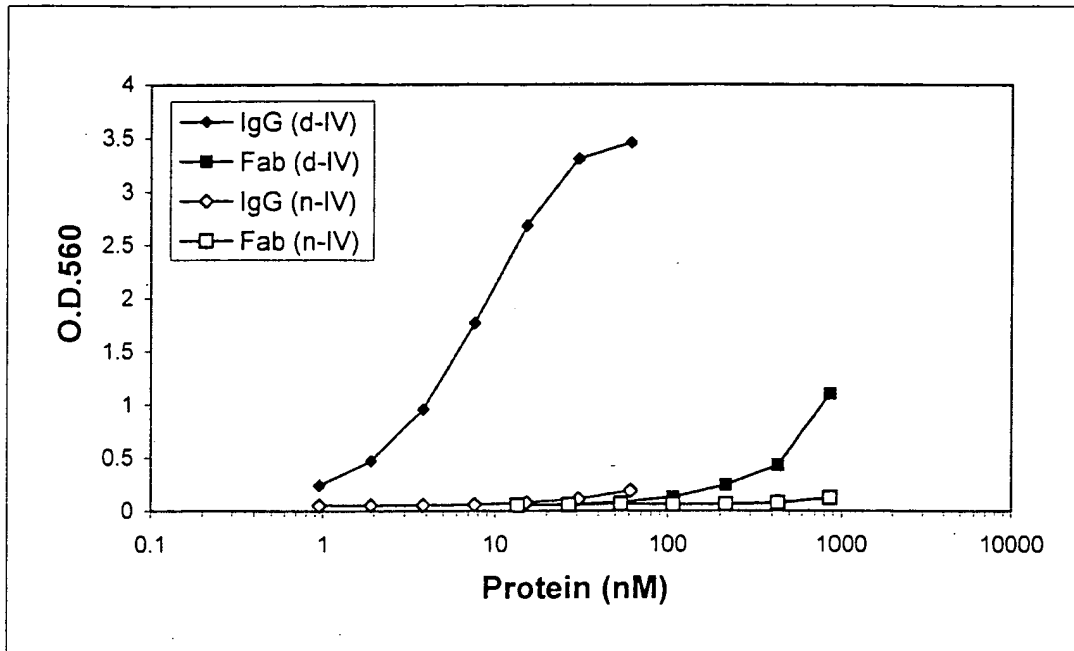


FIGURE 10

## Cell Proliferation (Cell Number)

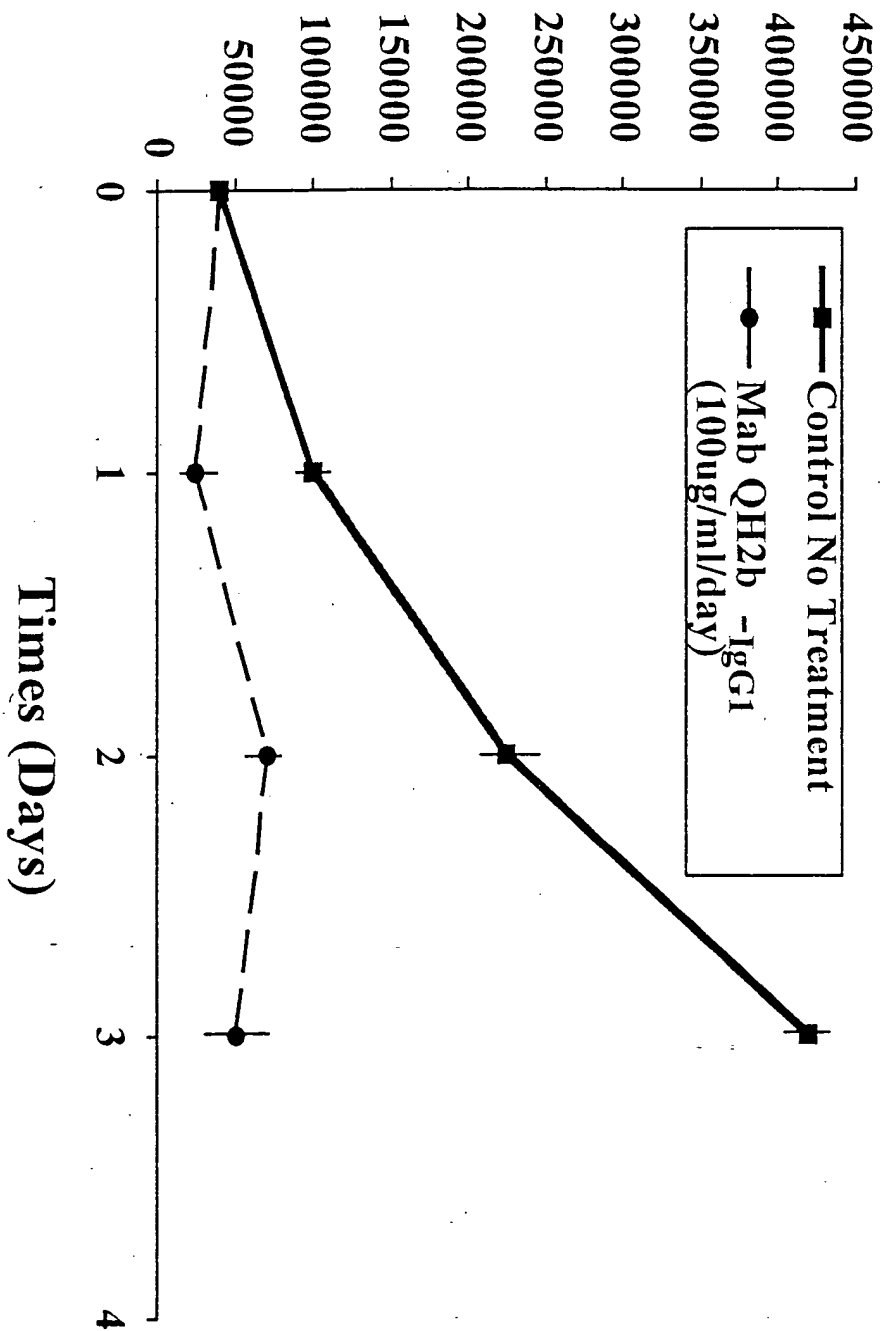


FIGURE 11